IN THE CLAIMS:

Applicants, pursuant to 37 C.F.R. § 1.121, submit the following amendments to the claims:

1. (Currently amended) A process for detecting the presence or absence of methylation of ~~a~~ CpG dinucleotide rich regions ~~region~~ of ~~a~~ nucleic acid sequences ~~sequence~~ within a genomic DNA sample ~~genome~~, the process comprising:

a)~~a.~~ contacting the genomic DNA sample ~~nucleic acid sequence~~ with an enzyme that is not methylation-sensitive, lacks a CpG dinucleotide sequence in its recognition motif, and that cleaves ~~which digests~~ the genomic DNA ~~nucleic acid sequences~~ into fragments in which CpG islands are preserved and which have ends corresponding to the cleavage motif of the non-methylation-sensitive enzyme;

b)~~b.~~ ligating ~~attaching~~ the fragments, via the ends corresponding to the cleavage motif of the non-methylation sensitive enzyme, to linker primers to form linker primer fragments ~~products~~;

c)~~c.~~ contacting the linker primer fragments ~~products~~ with a methylation-sensitive enzyme which digests the linker primer fragments ~~products~~ having unmethylated CpG dinucleotide sequences but not methylated CpG dinucleotide sequences to form a digestion product comprising methylated CpG island loci, and wherein fragments cleaved by the methylation-sensitive enzyme are rendered non-amplifiable by the linker primers;

d)~~d.~~ amplifying the digestion product to form amplicons of the methylated CpG island loci;

e)~~e.~~ labeling the amplicons;

f)~~f.~~ contacting the labeled amplicons with a screening array comprising a plurality of nucleic acid fragments affixed to a solid support; and

g)~~g.~~ determining the presence or absence of labeled amplicons bound to the plurality of nucleic acid fragments affixed to the solid support of the screening array to thereby detect the presence or absence of methylation of a CpG dinucleotide rich regions.

2. (Original) The process of claim 1 wherein the plurality of nucleic acid fragments affixed to the solid support of the screening array are derived from a CpG dinucleotide rich genomic library.

3. (Currently amended) The process of claim 2 wherein the plurality of nucleic acid fragments affixed to the solid support of the screening array are CpG dinucleotide rich fragments which comprise a sequence of at least about 200 nucleotides of which at least about 50% are guanine and cytosine.

4. (Original) The process of claim 3 wherein at least 20 nucleic acid fragments are affixed to the solid support of the screening array.

5. (Original) The process of claim 3 wherein the plurality of nucleic acid fragments affixed to the solid support of the screening array each contain a promoter and a first exon of a gene.

6. (Original) The process of claim 5 wherein the plurality of nucleic acid fragments affixed to the solid support of the screening array each comprise a nucleic acid sequence which is expressed in an organism.

7. (Original) The process of claim 6 wherein at least 20 nucleic acid fragments are affixed to the solid support of the screening array.

8. (Original) The process of claim 7 wherein at least 100 nucleic acid fragments are affixed to the solid support of the screening array.

9. (Original) The process of claim 8 wherein at least 500 nucleic acid fragments are affixed to the solid support of the screening array.

10. (Original) The process of claim 1 wherein the solid support of the screening array comprises nylon, glass or silicon.

11. (Original) The process of claim 1 wherein the label is selected from the group consisting of radioisotopes and fluorescent labels.

12. (Original) The process of claim 1 wherein the enzyme is selected from the group consisting of MseI, Tsp509I, NlaIII and BfaI and the methylation sensitive enzyme is selected from the group consisting of BstU I, SmaI, SacII, EagI, 5 MspI, HpaII, HhaI and BssHII.

13. (Original) The process of claim 12 wherein the enzyme is MseI and the methylation sensitive enzyme is BstU I.

14. (Original) The process of claim 1 wherein said process is used for diagnosing and monitoring the prognosis of a disease associated with aberrant DNA methylation.

15. (Original) The process of claim 14 wherein said disease is breast cancer, prostate cancer, colon cancer, lung cancer, liver cancer and ovarian cancer.

16. (Original) The process of claim 15 wherein the disease is breast cancer.

17. (Original) The process of claim 16 wherein the CpG island fragments affixed on the solid support of the screening array comprise a fragment corresponding to ~~are selected from SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO : 4, SEQ ID NO: 5 , SEQ ID NO: 6 , SEQ ID NO: 7 , SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID N0: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35,~~ SEQ ID NO: 36~~, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45 and SEQ ID NO. 46~~.

Claims 18-80 (Cancelled)